

GenCore version 5.1.4_p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 1, 2003, 08:51:06 ; Search time 23.5 Seconds
(without alignments)
3478.165 Million cell updates/sec

Title: US-09-768-781-2
Perfect score: 2543
Sequence: 1 agaacacacagaccacacaa.....caaggcaagtgctgtctga 1389

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09768781/runat_01042003_084731_4968/app_query.fasta_1.1543
-DB=Issued Patents AA -QPMT=faetan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768781 @CEN 1 1 28 @runat_01042003_084731_4968 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	6.6	129	3	US-09-058-489-46
2	114	4.5	800	4	US-09-134-001C-5655
3	103.5	4.1	290	4	US-09-134-001C-4893
4	98.5	3.9	451	4	US-09-134-001C-4420
5	96.5	3.8	357	1	US-08-612-886-5
6	96.5	3.8	357	1	US-08-361-806A-5
7	96.5	3.8	357	5	PCT-US95-16806A-5
8	96.5	3.8	683	4	US-09-134-001C-5576
9	96	3.8	371	1	US-08-415-818-6
10	96	3.8	371	2	US-08-894-236-6
11	96	3.8	371	2	US-08-919-624-4
12	96	3.8	371	5	PCT-US96-01444-6

13	96	3.8	498	2	US-08-660-963-12	Sequence 12, Appl
14	95.5	3.8	255	2	US-09-154-802-3	Sequence 3, Appl
15	95.5	3.8	255	3	US-09-373-029-3	Sequence 3, Appl
16	95.5	3.8	325	3	US-08-706-281A-18	Sequence 18, Appl
17	95.5	3.8	325	4	US-09-097-231-18	Sequence 18, Appl
18	95	3.7	458	4	US-08-487-596-16	Sequence 16, Appl
19	92.5	3.6	325	1	US-08-671-525B-10	Sequence 10, Appl
20	92.5	3.6	325	1	US-08-672-109B-10	Sequence 10, Appl
21	92.5	3.6	325	2	US-08-842-045-10	Sequence 10, Appl
22	92.5	3.6	325	2	US-08-842-238-10	Sequence 10, Appl
23	92.5	3.6	325	3	US-08-629-335B-10	Sequence 10, Appl
24	92	3.6	944	4	US-09-134-001C-4352	Sequence 4352, Ap
25	90.5	3.6	378	3	US-09-239-843A-66	Sequence 66, Appl
26	90.5	3.6	378	4	US-09-088-337B-66	Sequence 66, Appl
27	89.5	3.5	382	4	US-09-262-477-2	Sequence 227, Ap
28	89.5	3.5	443	4	US-09-134-001C-3227	Sequence 3227, Ap
29	88.5	3.5	383	1	US-08-196-989B-4	Sequence 4, Appl
30	88.5	3.5	383	2	US-08-760-936-4	Sequence 4, Appl
31	88.5	3.5	480	1	US-09-041-075A-5	Sequence 5, Appl
32	88.5	3.5	1260	4	US-09-245-041-2	Sequence 2, Appl
33	88	3.5	370	1	US-08-415-818-12	Sequence 12, Appl
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35	88	3.5	370	5	US-08-467-948A-2	Sequence 2, Appl
36	87.5	3.4	296	2	US-08-467-948A-2	Sequence 2, Appl
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38	87	3.4	445	4	US-09-134-001C-3507	Sequence 50, Appl
39	87	3.4	1843	4	US-09-413-814-50	Sequence 2, Appl
40	86.5	3.4	378	4	US-09-082-088-2	Sequence 2, Appl
41	86.5	3.4	378	4	US-09-546-117-2	Sequence 2, Appl
42	86.5	3.4	382	4	US-09-542-733-2	Sequence 2, Appl
43	86.5	3.4	3079	5	PCT-US94-00198-4	Sequence 4, Appl
44	86	3.4	317	1	US-08-118-270-6	Sequence 6, Appl
45	86	3.4	317	5	PCT-US93-08528-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-058-489-46
; Sequence 46, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; TITLE OF INVENTION: the Y Chromosome
; FILE REFERENCE: WHI97-08PA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-058-489-46

Alignment Scores:
Pred. No.: 7.49e-11 Length: 129
Score: 169.00 Matches: 46
Percent Similarity: 56.82% Conservative: 29
Best Local Similarity: 34.85% Mismatches: 45
Query Match: 6.65% Indels: 12
DB: 3 Gaps: 2

US-09-768-781-2 (1-1389) x US-09-058-489-46 (1-129)

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Db 6 SerileAlaaspAspIlePheProLeuileSer-CysValGlyAlaIleHisCysAsnII 25

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RESULT 2
; Sequence 5655, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5655
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5655
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Score: 114.00 Matches: 96
Percent Similarity: 40.14% Conservative: 81
Best Local Similarity: 21.77% Mismatches: 135
Query Match: 4.48% Indels: 129
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Db 422 pGlnTyrGlyPheValLeuThrPhe---ValIleIleSerIleGlyValIleAlaSerI 441
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Qy 792 CACT-----TCCCGCTCTCTGATTTCTGTGTGCTC-----TT 821
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Db 642 eSerLeuIlePheIleArgGlnArgLeuThrMetValValLeuAsnGlyMetIleGlyPh 662
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Qy 822 CTCAGCCACTTTGAATTGAAGGTGTG-----CCCTTCTCTAGTCTCAACTTCTGAT 875
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Db 662 eAlaValThrLeuTyrPheIleAlaMetLysAlaProAspLeuAlaLeuThrGlnLeuVa 682
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Qy 876 CATCTCTTTGAGCCCTGGATTAAAGTCTCTGGAGAGTGGTCCCGCAGATGCCCAAT----- 930
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Db 702 oArgValLysAlaAsnLeuLysLysGluThrPheLysIleIleValSerLeuValMetAl 722
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Qy 975 GATTTC---GTCACCATCTCTATGTGGGATCAACTCTCTTCTGCTGCTAGCTTTGCA 1031
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Db 722 aLeuThrValValSerLeuIlePheValAlaGlnAlaAspGlyMetProSerIleAl 742
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Qy 1032 GTTGAGGTGGCAGACAGAGATCTCTGTCGACAAAGGCGAGAACTGGGACATATGGGCT 1091
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Db 742 aLysPheTyrGluAspAlaTyrGluLeuThrGlyGlyLysAsn----- 756
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Db 757 -----IleValAsnAlaIleLeuGlyAspPheArgAlaLeuAspTh 770
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Qy 1126 -----ATGGTCTTGGTTTTTAAGTCTCTTGGAGTGAAGTGTACTGATTA 1172
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Db 770 rMetPheGluGlyLeuValLeuIleAlaGlyLeuGlyIleTyrThrLeuLeuAsnTyr 790
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Qy 1173 C 1173

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QY 424 CAGGAGGAGCCCTATGTGAGC----- 444
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QY 445 -----CTCACCCGAAAGAGATGCTAATAGATGCGAGGAGTGTCTGATAGATGGAG 498
Db 197 IleValIleAlaProLysSerTyrLeuIleAspGluSerLeuArgSerValPheLys 216
QY 499 GTGGGCACTCCATCCGAGCCCTGGCTATGACCCCAATGCTCAAAAGGATGTACAG 558
Db 217 AspAlaHisSerPheAlaValIleLeu-----AlaMetGlyLeu 229
QY 559 ATCCAAGCCTCTCTGGGCTAGTCCGAGCTGACCTATCAGCTCTATGTAGCCTGATC 618
Db 230 ValLeuTyrMetValThrIleIleLysGlnAspTyrAspValPheAsnLeuLeuLeu 249
QY 619 TCTCAGAGGTTCCCTGGGAGAGTGTCTGAATGTATTTCCCTGCTATCTGTACCC 678
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QY 679 TATGGGCACTCTTGGCAATATGTTGCTATCCAGATCAAGTAGGATGACTACAGATT 738
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QY 739 CGC-----CTTGGGCCACTAGAGTCTCTGCTCATCACCATCTGGGGACATTGGAG 789
Db 287 LysHisProIleIleGlyAlaMetIleLeuMetAlaIleAlaIle-----TTC 822
QY 790 ATCACTTCCCGCCTCTGATCTGTGTGTC----- 822
Db 307 IleTyrHisLeuPheIleLysLeuIleLysGlyLysAsnSerGlnGluValPheMet 326
QY 823 TCAGCCACTTTGAATGAAGCTGTG-----CCCTTCTCTAGTG 861
Db 327 ProSerAspMetAsnIleLysAlaIleAspTyrAlaLeuThrGluHisProPheLeuGly 346
QY 862 CTCAACTTCTGTATCATCTCTTTGAGCCCTGGATTAGTTCTGGAGAGTGGTCCCCAG 921
Db 347 SerGlyPheGlyIle-----ProMetIleLys----- 355
QY 922 ATGCCCAATACATTGAGAAAAAATTTCAGCGGGTCCGCACTCTGGTGGTCTGTGATTTC 981
Db 356 -----AlaSerSerGluIleGlnTyrPheAsnValAlaThrSerAsnIleIlePheGly 373
QY 982 GTACCAATCTCTATGTGGCATCAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041
Db 374 Met---IleIlePheThrGlyIle----- 380
QY 1042 GCACACAGAGATCTCGTCGACAAAGGGCAGAACTGGGGACATATGGGCTGCATATAGT 1101
Db 381 ----- 1101
QY 1102 GTGAGTTGGTAGAGATGTCATGCTGCTGTTTAAAGTCTTTGGAGTGAAGTG 1161
Db 387 ThrIleTyrMetLeuHisMetValLeuLeuValThrPhePro---MetSerIleThrIle 405
QY 1162 TTACTGAATTAATCTGTCATCTCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218
Db 406 LeuLeuPheLeuIleThrIlePheValAsnMetAspTyrIleIleLeuPheAspSerVal 425
QY 1219 TCCATTGGCTTCATGCTCTCTTCTTCCAGTACTTTCATTCATTCATTCATTCATTC 1278
Db 426 GlyLeuGlyIleLeuCysTyrIlePheTrpGlyIleTyrLeuLysGluGlyMetTyrGln 445
QY 1279 CATAAT 1284
Db 446 TyrAsn 447

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RESULT 5

US-08-612-986-5
; Sequence 5' Application US/08612986
; Patent No. 5770384

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; GENERAL INFORMATION:
; APPLICANT: Elliot J. Androphy
; APPLICANT: Dave E. Breiding
; TITLE OF INVENTION: E2 BINDING PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,986
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,806
; FILING DATE: 22 DEC 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-004DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-612-986-5

Alignment Scores:
Pred. No.: 0.0288 Length: 357
Score: 96.50 Matches: 35
Percent Similarity: 37.61% Conservative: 9
Best Local Similarity: 29.91% Mismatches: 56
Query Match: 3.79% Indels: 17
DB: 1 Gaps: 4

US-09-768-781-2 (1-1389) x US-08-612-986-5 (1-357)
QY 273 CATTATGTCAGTTGACCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCT 332
Db 220 HisTyrGlyProThrGlnProAlaTyrSerProSerGlnGlnLeuArgAlaProSerAla 239
QY 333 ATC-----ATTATTATGCACTAATCTCTTGGGACCTGTATCATCATGTTTGGAGCC 386
Db 240 PheProAlaValGlnTyrLeuSerGlnProGlnHisGlnProTyrAlaValHisGlyHis 259
QY 387 CATGATTAAGTACCTCACACTGTGTGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGG 446
Db 260 PheGln-----ProThrGlnThrGlyPheLeuGlnProGlyGlyAlaLeuSerLeuGln 277
QY 447 CACCGGAAGAAGATGCTAATAGATGCGAGAGAGTGTGTAGTAAGTGGAGGTGGGCCA 506
Db 278 LysGlnMetGluHisAlaAsnGlnGlnThrGlyPheSerAspSerSerSerLeuArgPro 297
QY 507 -----CTCCATCCGGACCCCTGCTATGACCCCAATGCTACCAACGTAT 551
Db 298 MethHisProGlnAlaLeuHisProAlaProGly-----Leu 309
QY 552 GTCACAGATCCAAGCCTTCTGGGCTCAGTGCCTCCAGCTGACCTATCAGCT 602
Db 310 LeuAlaSerProGlnLeuProValGlnMetGlnProAlaGlyLysSerAla 326

```

RESULT 6

US-08-361-806A-5
; Sequence 5, Application US/08361806A
; Patent No. 5,792833
; GENERAL INFORMATION:
; APPLICANT: Elliot J. Androphy
; APPLICANT: Dave E. Breiding
; TITLE OF INVENTION: E2 BINDING PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.806A
; FILING DATE: 22 DEC 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-361-806A-5

Alignment Scores:	
Pred. No.:	0.0288
Score:	96.50
Percent Similarity:	37.61%
Best Local Similarity:	29.91%
Query Match:	3.79%
DB:	1
Length:	357
Matches:	35
Conservative:	9
Mismatches:	56
Indels:	17
Gaps:	4

US-09-768-781-2 (1-1389) x US-08-361-806A-5 (1-357)

Qy	273	CATTATGGTCCAGTTGACCTCAATTTTGTGCCACAGAGATCTTAGCCAAAGATAAACCGT	332
Db	220	HisTyrGlyProThrGlnProIaTyrSerProSerGlnGlnLeuArgAlaProSerAla	239
Qy	333	ATC-----ATTATTTATGATCTAATCCCTCTGGGACCTGTTATCAGATGTTTGGAGGC	386
Db	240	PheProAlaValGlnTyrLeuSerGlnProGlnHisGlnProTyrAlaValHisGlyHis	259
Qy	387	CATGATTAACTACCTCACCTGGGAGAAAGAGGACGAGGAGGCCCTTATGTCAGCCT	446
Db	260	PheGln-----ProThrGlnThrGlyPheLeuGlnProGlyGlyAlaLeuSerLeuGln	277
Qy	447	CACCCGNAAGAAGATGCTATAGATGGCGAGGAGGTGCTGATAGAAATGGAGGTGGGCCA	506
Db	278	LysGlnMetGluHisAlaAsnGlnGlnThrGlyPheSerAspSerSerLeuArgPro	297
Qy	507	-----CTCCATCCGGACCTGGCTATGCACCGCAATGCCTACAAACGTAT	551
Db	298	MetHisProGlnAlaLeuHisProAlaProGly-----Leu	309
Qy	552	GTCAAGATCCAAAGCCTTCTGGGCTCAGTGCCGCCAGCTGACCTATCAGCT	602

Db 310 LeuAlaSerProGlnLeuProValGlnMetGlnProAlaGlyLysSerAla 326

RESULT 7

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PCT-US95-16806A-5
; Sequence 5, Application PC/TUS9516806A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: E2 Binding Proteins
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16806A
; FILING DATE: December 22, 1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/361,806
; FILING DATE: 22-DEC-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-16806A-5

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Alignment Scores:		
Pred. No.:	0.0288	357
Score:	96.50	35
Percent Similarity:	37.61%	Conservative: 9
Best Local Similarity:	29.91%	Mismatches: 56
Query Match:	3.79%	Indels: 17
DB:	5	Gaps: 4

US-09-768-781-2 (1-1389) x PCT-US95-16806A-5 (1-357)

Qy	273	CATTATGGTCCAGTGGACCTCATATTTTGTGCCACAGAGATCTTAGCCAAAGATAAACCGCT	332
Db	220	HisTyrGlyProThrGlnProAlaTyrSerProSerGlnGlnLeuAlaProSerAla	239
Qy	333	ATC-----ATTATTTATGCATCTAATCTCTCTGGGACCTGTTATCAGATCTTTTGAGGC	386
Db	240	PheProAlaValGlnTyrLeuSerGlnProGlnHisGlnProTyrAlaValHisGlyHis	259
Qy	387	CATGATTAACTACTCACACTGTGGGAAGAAGAGGACGAGGAGCCCTATGTCAGCCT	446
Db	260	PheGln-----ProThrGlnThrGlyPheLeuGlnProGlyGlyAlaLeuSerLeuGln	277
Qy	447	CACCCGAAAGAAGATGCTAATAGATGCGAGGAGGTGCTAGATAGAAATGGGAGGTGGGCCA	506
Db	278	LysGlnMetGluHisAlaAsnGlnGlnThrGlyPheSerAspSerSerSerLeuArgPro	297
Qy	507	-----CTCCATCCGGACCCCTGGCTATGCACCGCAATCCCTACAAACGCTAT	551
Db	298	MetHisProGlnAlaLeuHisProAlaProGly-----Leu	309
Qy	552	GTACAGATCCAAGCCTTCTCGGGCTCAGTGCCTCCAGCTACCTATCAGCT	602
Db	310	LeuAlaSerProGlnLeuProValGlnMetGlnProAlaGluValvsSerAla	326

RESULT 8

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US-09-134-001C-5576
; Sequence 5576, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCES: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134_001C

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;
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5576
; LENGTH: 683
; TYPE: PRN
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5576

Alignment Scores:
Pred. No.: 0.0415 Length: 683
Score: 96.50 Matches: 82
Percent Similarity: 38.50% Conservative: 77
Best Local Similarity: 19.85% Mismatches: 151
Query Match: 3.79% Indels: 103
DB: 4 Gaps: 19

US-09-768-781-2 (1-1389) x US-09-134-001C-5576 (1-683)

Qy 262 ATGTTTCATCATATGTCAGTCAGTCAGTCATTT-----TTTGTCCACAGA 309
Db 7 IlePheGluThrLeuLeuIlePheValAlaLeuValIleValSerSerPheValHisThr 26
Qy 310 GATCAGCCAAAGATAAACCCCTATCATTTATGTCATCTAACTCTTGGGACCTGTT 369
Db 27 PheIleProLys-----ValProLeuAlaPheIleGln-----IlePheLeuGly 41
Qy 370 ATCAGATGTTTGGAGGCCATGATTAAAGTACCTCACACTGTGGAGAAAGAG----- 420
Db 42 -----MetIleLeuTyrlleuThrProIleProValGluPheAsnPhe 55
Qy 421 GAGCAGAGGAGCCCTATGTCAGGCTCACCGAAGAGATGCTAATAGATGGGAGGAG 480
Db 56 AspSerGluLeuPheMetValThrLeuIleAlaProLeuLeuPheValGluGly----- 73
Qy 481 GTGCTGATAGATGGAGGTGGGCCACTCCATCCGACCCCTGGCTATGCACCGCAATGCC 540
Db 74 -----ValAsnValSerArgValHisLeuArgLys 83
Qy 541 TACAAAGCTATGTACAGATCCAGACCTCTCTGGGCTCAGTG-----CCCGCAGTCACC 594
Db 84 TyrlleLysProValMetMetMetAla---LeuGlyLeuValIleThrValIleGly 102
Qy 595 TATCAGCTCTATGAGGCTGATCTCTCGAGAGGTTCCTGGGTAGAGTGTGTCTAATG 654
Db 103 ValGlyLeuPheIleHisTrpIleTrpProGluLeuProIleGlyAlaAlaPheAlaIle 122
Qy 655 GTATTTTCCCTG----- 666
Db 123 AlaAlaIleLeuCysProThrAspAlaValAlaValGlnAlaIleThrLysGlyLysVal 142
Qy 667 -----GTATCTGTACCTATGCGGCCACCTTTGCAATATGTTGGCTATC 711
Db 143 LeuProLysGlySerMetThrIleLeuGluGlyGluSerLeuLeuAsnAspAlaIleGly 162
Qy 712 CAGATCAAGTACGATGACTACAGATTCGCTCGGCGCCACTAGAGTCTCTGCATCACC 771
Db 163 IleIle-----SerPheLysIleAlaValGlyValLeuIleThrGlyThrPheSer 179
Qy 772 ATCTGGGGGACATTTGGAG-----ATCACTTCC-----CGCTTC 804
Db 180 IlePheAspAlaIleGlnGlnPheLeuIleAlaSerIleGlyAlaIleValGlyLeu 199
Qy 805 CTGATT-----CTGGTCTCTTCTCAGCCACTTTGAAATTTGAAGCTGTGCCCTTC 855
Db 200 IleIleGlyMetAlaLeuValArgPheArgLeuThrMetArgArgGlyIleLeuAsn 219
Qy 856 CTAGTGTCTCACTTCTCTGATCATCTCTTCTGAGCCCTGGATTAAGTCTTGGAGAGTGGT 915
Db 220 IleAsnMetPheThrPheIleGlnLeuLeuThrProPheValThrTyrlleu----- 236

Qy 916 GCCCAGATGCCCAATAACATTGAGAAAACTTCAGCCGGGTGGCAGCTCTGTGTGCTCTG 975
Db 237 -----IleAlaGluLeuPheHisAlaSerGlyIleIleAlaAlaVal 250
Qy 976 ATTTCAATCACCATCCTCTATGCTGGCATCACTTCTCTGCTGCTGCTGCTGCTGCTG 1035
Db 251 Val-----AlaGlyLeu-----Val 255
Qy 1036 AGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTGGGGACATATGGCGCTGCAC 1095
Db 256 HisGlyPheGluArgAspArgIleAlaGlnThrArgThrGlnLeuGlnMetSerTyrlleu 275
Qy 1096 TATAGTGTGAGTTGGTAGAGAATGTGATCATGTGCTTGGTGTGTTTAAAGTCTTTCGA--- 1152
Db 276 HisThrTrpSerIleLeuGlyTy-ValLeuAsnGlyPheValPheSerIleLeuGlyPhe 295
Qy 1153 -----GTCAAAGTGTACTGTAATTAATGCTCATCTCTGATTCCTGATTCGCTTG 1194
Db 296 LeuValProGluValIleValIleValIleLysThrGluProHisAsnLeuLeuPheLeu 315
Qy 1195 CAGCTCATATTGCTTATCTGATTTCCATTTCCATTTGCTTTCATGCTCTCTTCTTCCAGTACTTG 1254
Db 316 ---IleValIleThrLeuLeuValAlaLeuAlaValTyrlleuPheArgPheValIleVal 334
Qy 1255 CATCATTTGCTCCTCTTCCACCATTAATGTAGTAGACTACCTCCATTTGCTGCTGCTGT 1314
Db 335 TyrlleuLeuTyrlleuTyrlleuTyrlleuTyrlleuTyrlleuTyrlleuTyrlleu 352
Qy 1315 CACCAGCACCTCGGACCGAGGTTGAGAACTCAGAGCCA 1353
Db 353 SerLysAsnAspGluAspLysValThrGluSerLysPro 365

RESULT 9

US-08-415-818-6
; Sequence 6, Application US/08415818
; Patent No. 5621079
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,818
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720

: INFORMATION FOR SEO ID NO: 6:

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; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-818-6

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Alignment Scores:

pred. No.:	0.0336	Length:	371
Score:	96.00	Matches:	78
Percent Similarity:	37.39%	Conservative:	85
Best Local Similarity:	17.89%	Mismatches:	153
Query Match:	3.78%	Indels:	120
DB:	1	Gaps:	18

US-09-768-781-2 (1-1389) x US-08-415-818-6 (1-371)

QY	116	GAGCAACCCCGAT-----TTACTTTTCCATTATGCA	148
DB	7	GlnProThrProLeuLysThrSerGlyLysSerAsnAsnSerAlaPhePheTyrGlyGlu	26
QY	149	TCCTTTTCTCCACCTTTTGTGTACTGTGGGAGGCTGCATCTGCTTTGTGTACATGGTTAGAA	208
DB	27	SerCysGlnProProPheLeuAlaLeu-----LeuLeuLeuLeuLeuAlaTyr	42
QY	209	TCTATCGAAAGAATAGTGAACACTTACTGGATGACATACACCTTTTCTTTCTTTATGTTTT	268
DB	43	ThrValIleLeuIleMetGlyIlePheGly-AsnLeuSerLeuIleIleIleIle-----	60
QY	269	CATCCATTATGGTCCAGTTCACCTCATTTTGTCTCCACAGAGATCTAGCGCAAGATAAAC	328
DB	61	-----PheLysLysGlnArgGluAlaGlnAsnValTh	71
QY	329	CGCTATCATTTATT-----TATGCATCTAATCTCTTGGGACCTGTTATCAGATGTTTCG	382
DB	71	raenIleLeuIleAlaAsnLeuSerAspIleLeuValCys-ValMetCysIleSp	91
QY	383	AGGCATGATTAAGTACTCTCACACTGTGGGAAGAAAGGAGGAGGAGGCCCTATGTCA	442
DB	91	roPheThrValIleTyr-----	96
QY	443	GCCTCACCCGAAGAGATGCTAATATAGATCGCGAGGAGGTGCTCATAGTAATGGAGGTGG	502
DB	97	-----ThrLeuMetAsp-----HisTrpValPheG	105
QY	503	GCCACTCCATCCGAGCCCTGGCTATGCAACCGCAATGCTACAAACGATGTATCACAGATCC	562
DB	105	lyAanThrMetCysLysLeu-----ThrSerTyrValGlnSerValSerValS	121
QY	563	AGCCTTCCTGGGCTAGTGGCCCGCAGCTGACCTATCAGCTCTATGTGAGCGTGATCTCTG	622
DB	121	erValSerIlePheSerLeuValLeuIleAlaIleGluArgTyrGlnLeuIleValAsnP	141
QY	623	CAGAGGTTCCTCCCTGGGTAGAGTTGTG-----CTAATGGTATTTCCTCCCTGG	667
DB	141	roArgGlyTyrLysProArgValAlaHisAlaTyrTrpGlyIleIleLeuIleTrpLeu	161
QY	668	TATCTGTCACTATGGGGCCACCTTTGGCAATATGTTGGCTATCCAGATCAAGATCAGATG	727
DB	161	leSerLeuThrLeuSerIleProLeu-----PheLeuSerTyrHisLeuThrAsnGluP	179
QY	728	ACTACAAGATTCCGCTTGGGGCCACTA-----GAAGTCCTCTGCATCACCA	772
DB	179	roPheHisAsnLeuSerLeuProThrAspIleTyrThrHisGlnValAlaCysValGluI	199
QY	773	TCTGGCGGACATGTTGAGATCACTTCCCGCCTCTCGATTCTGGTGCCTCTCTCAGCCACT	832
DB	199	leItrProSer-----LysLeuAsnGlnLeuLeuPheSerThrSerL	213
QY	833	TGAATTGAAGGCTGTGCCCTTCTAGTGTCTCAACTTCCTGTGATCATCTCTTTGAGCCCT	892
DB	213	euPheMetLeuGlnTyr---PheValProLeuGlyPheIleLeuIleCysTyrLeuLysI	232

RESULT 10

US-08-894-236-6
; Sequence 6, Application US/08894236
; Patent No. 5939263
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,236
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,818
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3462
 TELEFAX: 908-594-4720
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 371 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-894-236-6

Alignment Scores:

Pred. No.: 0.0336 Length: 371
 Score: 96.00 Matches: 78
 Percent Similarity: 37.39% Conservative: 85
 Best Local Similarity: 17.89% Mismatches: 153
 Query Match: 3.78% Indels: 120
 DB: 2 Gaps: 18

US-09-768-781-2 (1-1389) x US-08-894-236-6 (1-371)

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Qy 116 GAGCAACCCCGAT-----TTACTTTTCCATTTAGCA 148
Db 7 GlnProThrProAsnLysThrSerGlyLysSerAsnAsnSerAlaPhePheTyrPheGlu 26
Qy 149 TCCCTTTTCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGGTTAGAA 208
Db 27 SerCysGlnProProPheLeuAlaIle-----LeuLeuLeuLeuLeuAlaTyr 42
Qy 209 TCTATCGAAAGATAGTAAACTTACTGTGATGACATACACCTTTCTTTCTTTATGTTTT 268
Db 43 ThrValIleLeuIleMetGlyIlePheGly-AsnLeuSerLeuIleIleIleIle----- 60
Qy 269 CATCCATTATGGTCAGTTGACCTTCATTTTGTCCAGAGATCTACGCCAAAGATAAAC 328
Db 61 -----PheLysLysGlnArgGluAlaGlnAsnValTh 71
Qy 329 CGCTATCATTTATT-----TATGCATCTAATCTCTTGGACCTGTTATCAGATGTTGG 382
Db 71 AsnIleLeuIleAlaAsnLeuSerLeuSerAspIleLeuValCys-ValMetCysIleP 91
Qy 383 AGGCATGATTAAAGTACCTCACACTGTGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGG 442
Db 91 roPheThrValIleTyr-----HisTrpValPheG 96
Qy 443 GCCTACCCGAAAGATGCTAATAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 502
Db 97 -----ThrLeuMetAsp----- 105
Qy 503 GCCACTCATCGGACCTGGCTATGACCGCAATGCCTACAAACGTATGTCACAGATCC 562
Db 105 LysThrMetCysLysLeu-----ThrSerTyrValGlnSerValSerValS 121
Qy 563 AAGCCTTCTGGGCTCAGTGCAGCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTGTG 622
Db 121 ervAlSerIlePheSerLeuValIleAlaIleGluArgTyrGlnLeuIleValAsn 141
Qy 623 CAGAGTTTCCCTGGGTAGAGTTGTG-----CTAATGGTATTTCCCTGG 667
Db 141 roAGlyTrpLysProArgValAlaHisAlaTyrTrpGlyIleIleLeuIleTrpLeu 161
Qy 668 TATCTGTACCATATGGGCGCCCTTTGTCATATGTTGGCTATCCAGATCAAGTACGATG 727
Db 161 leSerLeuThrLeuSerIleProLeu-----pheLeuSerTyrHisLeuThrAsnGlu 179
Qy 728 ACTACAGATTCCGCTTGGCCCACTA-----GAAGTCTCTGCATCACCA 772
Db 179 roPheHisAsnLeuSerLeuProThrAspIleTyrThrHisGlnValAlaCysValGlu 199
Qy 773 TCTGCGGACATATGGAGATCACTTCCCGCCTCTGATTTCTGCTCTTCTCAGCCACTT 832
Db 199 leTrpProSer-----LysLeuAsnGlnLeuLeuPheSerThrSerL 213

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Qy 833 TGAATTTGAAGGCTGTGCCCTTCTTAGTGCTCAACTTCTCTGATCATCTCTTTTGGACCT 892
Db 213 euPheMetLeuGlnTyr---PheValProLeuGlyPheIleLeuIleCysTyrLeuLysI 232
Qy 893 GGATTAAGTTCTGGAGAAGTGTGCCAGATGCCCAATAACATTGAGAAAAAATCTCAGCC 952
Db 232 leValLeuCysLeuArgLysArgThrArgGlnValAspArgArgLysGluAsnLysSerA 252
Qy 953 GGGTCGGC-----ACTCTGGTGGTCTCTATTTCAGTCACCATCTCTCTATGCTG 1000
Db 252 rgLeuAsnGluAsnLysArgValAsnValMetLeuIleSerIleValThrPheGly- 271
Qy 1001 GCATCAACTTCTTGTGTCGTGAGCTTTCAGTGTGAGGTTGGCAGACAGAGATCTCGTCG 1060
Db 272 -----AlaCysTrpLeuProLeuAsn----- 278
Qy 1061 ACAAGGCGCAAACTGGGACATATGGCCCTGCACATATAGTGTGAGGTTGGTAGAGAA 1120
Db 278 ----- 278
Qy 1121 TGATCATGCTCTTGGTTTTTAAGTTTCTTTGGAGTGAAAGTGTACTGAATTACTGTCA 1180
Db 279 --IlePheAsnValIlePheAspTrpTyrHis---GluMetLeuMetSerCysHisHisA 297
Qy 1181 CTTGATTGCTTGCAGCTCATATTATGCTTATCTGATTTCCATTGGCTTTCATGCTCTTT 1240
Db 297 spLeuValPheValValCysHisLeuIleAlaMetValSerThrCysIleAsnProLeuP 317
Qy 1241 TCTTCCAGTACTTCATCCATTGCGCTCAGCTCTTCCACCCATTAATAGTAGACTACCTCC 1300
Db 317 heTyrGlyPheLeuAsn-----LysAsnPheGlnLysAspLeuMetMetLeuIleH 334
Qy 1301 ATTGTGCTGTCTGCACGACGACCTCGGACCGAGGTTGAGAAC 1344
Db 334 leHisCysTrpCysGlyGlu---ProGlnGluSerTyrGluAsn 347

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RESULT 11

US-08-919-624-4
 ; Sequence 4, Application US/08919624
 ; Patent No. 5994097
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
 ; TITLE OF INVENTION: RECEPTOR
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/919,624
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0377 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 371 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1378004

; US-08-919-624-4

; Alignment Scores:

Pred. No.:	0.0336	Length:	371
Score:	96.00	Matches:	78
Percent Similarity:	37.39%	Conservative:	85
Best Local Similarity:	17.89%	Mismatches:	153
Query Match:	3.78%	Indels:	120
DB:	2	Gaps:	18

US-09-768-781-2 (1-1389) x US-08-919-624-4 (1-371)

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QY 116 GAGCCACCCCGAT-----TTACTTTTCCATTAGCA 148
Db 7 GlnProThrProAsnLysThrSerGlyLysSerAsnSerAlaPhePheTyrPheGlu 26
QY 149 TCCTTTTCTCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGGTTAGAA 208
Db 27 SerCysGlnProPheLeuAlaile-----LeuLeuLeuLeuLeuLeuAlaTyr 42
QY 209 TCTATCGAAGAAGATAGTGAACACTTACTGTGATGACATACACCTTTTCTTTTATATGTTT 268
Db 43 ThrValIleLeuIleMetGlyIlePheGly-AsnLeuSerLeuIleIleIleIle----- 60
QY 269 CATCCATTATGGTCCAGTTCACCTTCATTTTGTCCACAGAGATCTAGCCAAAGATAAAC 328
Db 61 -----PheLysLysGlnArgGluAlaGlnAsnValTh 71
QY 329 CGCTATCATATT-----TATGCATCTAATCCTCTGGGACCTGTTATCATAGATGTTGG 382
Db 71 rAsnIleLeuIleAlaAsnLeuSerLeuSerAspIleLeuValCys-ValMetCysIleP 91
QY 383 AGCCCATGATTAAATGATCACTCAGCTGTGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAG 442
Db 91 roPheThrValIleTyr-----HisTrpValPheG 502
QY 443 GCCTACCCGAAAGAGATGCTAATAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 502
Db 97 -----ThrLeuMetAsp-----HisTrpValPheG 105
QY 503 GCCACTCCATCCGACCCCTGGCTATGACCCGATGCTACAAACGATGATGCAGATCC 562
Db 105 lYAsnThrMetCysLysLeu-----ThrSerTyrValGlnSerValSerValS 121
QY 563 AAGCCTTCTCTGGGCTAGTGGCCCGAGCTACCTATCAGCTATGATGAGCTGATCTCTG 622
Db 121 erValSerIlePheSerLeuValLeuIleAlaIleGluArgTyrGlnLeuIleValAsn 141
QY 623 CAGAGGTTCCCTCGGTAGAGTTGTG-----CTAATGGTATTTTCCCTGG 667
Db 141 roArgGlyTyrLysProArgValAlaHisAlaTyrTrpGlyIleIleLeuIleTrpLeu 161
QY 668 TATCTGTACCTATGCGGCCACCCCTTTGCAATATGTTGGCTATCCAGATCAAGTACATG 727
Db 161 leSerLeuThrLeuSerIleProLeu-----PheLeuSerTyrHisLeuThrAsnGlu 179
QY 728 ACTACAAGATTGCGCTTGGGCGACTA-----GAAGTCTCTGCATCACA 772
Db 179 roPheHisAsnLeuSerLeuProThrAspIleTyrThrHisGlnValAlaCysValGlu 199
QY 773 TCTGGGAGCATTTGGAGATCACTTCCCGCCTCTCTGATTTCTGCTCTCTTCTCAGCCACTT 832
Db 199 leTrpProSer-----LysLeuAsnGlnLeuLeuPheSerThrSerL 213

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QY 833 TGAATTTGAAGGCTGTGCCCTTCTAGTGTCTCAACTTCTCTGATCATCTCTTTTGAGCCCT 892
Db 213 euPheMetLeuGlnTyr---PheValProLeuGlyPheIleLeuIleCysTyrLeuLysI 232
QY 893 GGATTAACTTCTGGAGAAGTGTGCCAGATGCCCAATAACATTAGAGAAAAAATTTCAGCC 952
Db 232 leValLeuCysLeuArgLysArgThrArgGlnValAspArgArgLysGluAsnLysSerA 252
QY 953 GGGTCGGC-----ACTCTGGTGGTCTCTATTTCACTCACCATCTCTCTATGCTG 1000
Db 252 rgLeuAsnGluAsnLysArgValAsnValMetLeuIleSerIleValValThrPheGly- 271
QY 1001 GCATCAACTTCTCTGCTGGTCAGCTTTGCGAGTTGAGGTTGGCAGACAGAGATCTCGTCG 1060
Db 272 -----AlaCysTrpLeuProLeuAsn----- 278
QY 1061 ACAAGGCGAAGACTGGGACATATGGGCGCTGCACATATAGTGTGAGGTTGGTAGAATG 1120
Db 278 ----- 278
QY 1121 TGATCATGGCTCTTGGTCTTTAAAGTTCTTTGGAGTGAAGTGTACTGAATTACTGTCAAT 1180
Db 279 --IlePheAsnValIlePheAspTrpTyrHis---GluMetLeuMetSerCysHisHis 297
QY 1181 CTTGATTCCTTCGAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCTTT 1240
Db 297 spLeuValPheValValCysHisLeuIleAlaMetValSerThrCysIleAsnProLeuP 317
QY 1241 TCTTCCACTACTTCATCTCATTGGCTCCTCTTCCACCCATAATAGTAGAGACTACCTCC 1300
Db 317 heTyrGlyPheLeuAsn-----LysAsnPheGlnLysAspLeuMetMetLeuIleH 334
QY 1301 ATTGTGTCTGCTGCACGACGACCTCGGACGAGGTTGAGAAC 1344
Db 334 iHisCysTrpCysGlyGlu---ProGlnGluSerTyrGluAsn 347

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RESULT 12

PCT-US96-01444-6

; Sequence 6, Application PC/TUS9601444

; GENERAL INFORMATION:

; APPLICANT: Cascieri, Margaret A.

; APPLICANT: Linemeyer, David L.

; APPLICANT: MacNeil, Douglas J.

; APPLICANT: Shiao, Lin-Lin

; APPLICANT: Strader, Catherine D.

; APPLICANT: Tan, Carina P.

; APPLICANT: Weinberg, David H.

; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mary A. Appollina

; STREET: P.O. Box 2000, 126 E. Lincoln Ave.

; CITY: Rahway

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/01444

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/383,746

; FILING DATE: 03-FEB-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/415,818

; FILING DATE: 03-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Appollina, Mary A.

REGISTRATION NUMBER: 34,087
 REFERENCE/DOCKET NUMBER: 19390Y
 TELEPHONE: 908-594-3462
 TELEFAX: 908-594-4720
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 371 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-01444-6

Alignment Scores:
 Pred. No.: 0.0336 Length: 371
 Score: 96.00 Matches: 78
 Percent Similarity: 37.39% Conservative: 85
 Best Local Similarity: 17.89% Mismatches: 153
 Query Match: 3.78% Indels: 120
 DB: 5 Gaps: 18

US-09-768-781-2 (1-1389) x PCT-US96-01444-6 (1-371)

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Qy 116 GAGCAACCCCGAT-----TTACTTTTCCATTAGCA 148
   |||||
Db 7 GlnProThrProAsnLysThrSerGlyLysSerAsnAsnSerAlaPhePheTyPheGlu 26

Qy 149 TCCTTTTCTCACCTTTTGTACTGTGGGAGGCTGCTGCTTTGTACATGGTTAGAA 208
   |||||
Db 27 SerCysGlnProPheLeuAlaile-----LeuLeuLeuLeuLeuAlaTyr 42

Qy 209 TCATCGAAGAAAGTAGCAACTTACTGATGATGACATACACCTTTTCTTTTATGTTT 268
   |||||
Db 43 ThrValLeuLeuLeuMetGlyPheGly-AsnLeuSerLeuLeuLeuLeuLeuLeu 60

Qy 269 CATCCATTATGGTCCAGTGTGACCTTCATTTTGTCCAGAGATCTAGCCAAAGATAAAC 328
   |||||
Db 61 -----PheLysLysGlnArgGluAlaGlnAsnValTh 71

Qy 329 CGCTATCATTAATT-----TAGCATCTAACTCTTGGACCTGTTATCATAGATTTGG 382
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Db 71 rAsnLeuLeuLeuAlaAsnLeuSerLeuSerAspLeuValCys-ValMetCysIleP 91

Qy 383 AGGCATGATTAACTACCTCACCTGTGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 442
   |||||
Db 91 roPheThrValIleTyr----- 96

Qy 443 GCCTCACCGAAGAGATGCTAATAGATGGCGAGGAGTCTGATAGATGGGAGGTGG 502
   |||||
Db 97 -----ThrLeuMetAsp-----HisTrpValPheG 105

Qy 503 GCCACTCCATCCGACCTGCTATGACCCGAAATGCTTACAAACGTATGTACAGATCC 562
   |||||
Db 105 lYAsnThrMetCysLysLeu-----ThrSerTyrValGlnSerValSerValS 121

Qy 563 AAGCTTCTGGGCTCAGTCCGACGAGTACCTATACGCTCTATGTGAGCCGTGATCTGTG 622
   |||||
Db 121 erValSerIlePheSerLeuValLeuLeuAlaIleGluArgTyrGlnLeuIleValAsn 141

Qy 623 CAGAGGTTCCCTGGGTAGAGTTGTG-----CTAATGGTATTTTCCCTGG 667
   |||||
Db 141 roArgGlyTrpLysProArgValAlaHisAlaTyrTrpGlyLeuLeuLeuLeuTrpLeu 161

Qy 668 TATCTGTACCTATGGGACCCCTTGTCAATATGTTGGCTATCCAGATCAAGTACGATG 727
   |||||
Db 161 leSerLeuThrLeuSerIleProLeu-----PheLeuSerTyrHisLeuThrAsnGlu 179

Qy 728 ACTACAAGATTGGCTTGGGCACTA-----GAAGTCTCTGCATCACC 772
   |||||
Db 179 roPheHisAsnLeuSerLeuProThrAspIleTyrThrHisGlnValAlaCysValGlu 199

Qy 773 TCTGGCGACATGGAGATCACTCCCGCTCTGATTCGTGCTCTTCTCAGGCACCTT 832
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Db 199 leTrpProSer-----LysLeuAsnGlnLeuLeuPheSerThrSerL 213
Qy 833 TGAATTAAGGCTGTGCCCTTCTAGTGTCTCAACTTCTCTGATCATCTCTTTTGAGCCCT 892
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Db 213 euPheMetLeuGlnTyr-----PheValProLeuGlyPheIleLeuIleCysTyrLeuLysI 232
Qy 893 GGATTAAGTCTGGAGAGTGGTCCCGAGATGCCCAATAAATGAGAGAAAATCTTCAGCC 952
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Db 232 leValLeuCysLeuArgLysArgThrArgGlnValAspArgArgLysGluAsnLysSerA 252
Qy 953 GGGTCGGC-----ACTCTGGTGGTCCCTGATTTCCAGTCCACCATCTCTATGCTG 1000
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Db 252 rgLeuAsnGlnAsnLysArgValAsnValMetLeuIleSerIleValThrPheGly- 271
Qy 1001 GCATCAACTTCTCTTGTGCTGTCAGCTTTCAGAGTTGAGGTTGGCAGACAGAGATCTCGTG 1060
   |||||
Db 272 -----AlaCysTrpLeuProLeuAsn----- 278
Qy 1061 ACAAGGCGAAGACTGGGACATATGGGCTGCACTATAGTGTGAGGTGGTAGAGATG 1120
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Db 278 ----- 278

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Db 279 --IlePheAsnValIlePheAspTrpTyrHis---GluMetLeuMetSerCysHisHisA 297
Qy 1181 CCTTGATTCCTTCAGCTCATTTATTTGCTTATCTGATTTCCATTGGCTTCATGCTCTTT 1240
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Db 297 spLeuValPheValValCysHisLeuLeuAlaMetValSerThrCysIleAsnProLeuP 317
Qy 1241 TCTTCCAGTACTTGCATCCATTGGCTCCTCTTCCACCCATAATGTAGTAGACTACCTCC 1300
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Db 317 heTyrGlyPheLeuAsn-----LysAsnPheGlnLysAspLeuMetMetLeuLeuH 334
Qy 1301 ATTGTGCTGCTGCACCGACCCCTCGGACCCAGGCTTGAGAAC 1344
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Db 334 lHisCysTrpCysGlyGlu---ProGlnGluSerTyrGluAsn 347

RESULT 13
US-08-660-963-12
; Sequence 12, Application US/08660963
; Patent No. 5852187
; GENERAL INFORMATION:
; APPLICANT: Thorne, Michael O.
; APPLICANT: Gaylinn, Bruce D.
; APPLICANT: Horikawa, Reiko
; APPLICANT: Lyons Jr., Charles E.
; TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,963
; FILING DATE: 12-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Shaughnessy, Brian P.
; REGISTRATION NUMBER: 32,747
; REFERENCE/DOCKET NUMBER: 18046.036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000

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Qy	706	GCTATCCAGATCAAGTACGACTACAAGATTGCCTTTGGGCCCACTAGAAGTCTCTTCG	765
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Qy	826	GCACATTGAAGCTGTGCCCTTCCTTAGTGCTCAACTCTCTCATCATCTCTTT	885
Dd	295	-----	295
Qy	886	GAGCCCTGGATTAAAGTTCTGGGAAAGTGGTCCCAGATGC	927
Dd	296	-----ProAlaCySGlyTrpValAlaSerTrpPr	305
Qy	928	AATA- - - - -ACATTGAGAAAACTTCAGCCGGTCGGCACT	963
Dd	305	oLeuLyMetLeuArgAlaGlyThrTrpThrAlaProProThrGlyGlySerSer	324
Qy	964	CTGGTGCTCGATTTCAGTCAACATCTCTTANGTGGCATCACT	1011
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Qy	1072	AACCTGGGGACATA- - - - -	1084
Dd	359	uSerThrGlyValSerLeuSerGlnArgPheSerSerPheArgCysLeuGluSerThrMe	379
Qy	1085	- - - - -TGGGCTCGCACTATAGTGTGAGTTGG- - -TAGAAGATGTCATCATGTCT	1131
Dd	379	tSerPheSerThrSerCysLeuThrValLeuGlyTrpThrSerAlaSerProAsnTrpAs	399
Qy	1132	TTGGTTTTTAAGTCTCTTTGGAGTGAAAGTTACTGTAATTACTGTTCATCTCTGATTGCC	1191
Dd	399	pTrpAlaLeuSerArg- - - - -	404
Qy	1192	TTGCAGCTCATATTGCTTATCTGATTTCCATGGCTTCATGCTCTTTTCTTCC- - -	1246
Dd	405	- - - - -AlaSerLeuLeuLeu- - - - -SerCysThrAlaSerSerThrLy	417
Qy	1247	- - - - -AGTACTTGCATCCATTGGCGTCACTCTTC	1275
Dd	417	sArgGlyLeuArgSerHisGlyAspGlyThrAlaThrIleLeuAsnPheCysGlnProGl	437
Qy	1276	ACCATAAATGTAGTAGACTTACCTCCATTGTCTGCTGCTCACACAGACACC- - -CTCGGACC	1332
Dd	437	yGlyLeuIleSerSerGluAspSerArgValIlyvalLeuThrSerValCysAlaGlyGl	457
Qy	1333	AGGGTTGAGAACTCAGAGCCACCT	1357
Dd	457	nSerLeuArgLeuGluProThrPro	465


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QY 1165 CTGAATTACTGTCATTCTTCCTTCGATTCGCTTCGAGCTCATTATTGCTTATCTGATTTCCATT 1224
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QY 1225 GGCTTCATGCTCCTTTTCTTCCAGTACTTG 1254
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Db 239 ValPheThrMetLeuThrCysSerTyrIle 248
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Search completed: April 1, 2003, 09:00:02
Job time : 34.5 secs